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Genetic diversity in wild sweet cherries (*Prunus avium*) in Turkey revealed by SSR markers

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ABSTRACT. Wild sweet cherry (*Prunus avium*) trees are abundant in the northern part of Turkey, including the Coruh Valley. We analyzed 18 wild sweet cherry genotypes collected from diverse environments in the upper Coruh Valley in Turkey to determine genetic variation, using 10 SSR primers. These SSR primers generated 46 alleles; the number of alleles per primer ranged from 3 to 7, with a mean of 4.6. The primer PS12A02 gave the highest number of polymorphic bands (N = 7), while CPSCT010, UDAp-401 and UDAp-404 gave the lowest number

(N = 3). Seven groups were separated in the dendrogram, although most of the genotypes did not cluster according to phenological and morphological traits. This level of genetic diversity in these wild sweet cherry genotypes is very high and therefore these trees would be useful as breeders for crosses between cultivated sweet cherry and wild genotypes.

Key words: Genetic diversity; SSR markers; Microsatellites; Wild sweet cherry

